

GPR64 NUCLEOTIDE SEQUENCE (SEQ ID NO: 1)

Gene name: G protein-coupled receptor 64
Unigene number: Hs.421137
Probeset Accession #: AA435577
Nucleic Acid Accession #: NM_005756.1
Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
AGCCAGCCCG	AGGACGCGAG	CGGCAGGTGT	GCACAGAGGT	TCTCCACTTT	GTTTTCTGAA	60
CTCGCGGTCA	GGATGGTTTT	CTCTGTCAGG	CAGTGTGGCC	ATGTTGGCAG	AACTGAAGAA	120
GTTTTACTGA	CGTTCAAGAT	ATTCTTGTC	ATCATTTGTC	TTCATGTCGT	TCTGGTAACA	180
TCCCTGGAAG	AAGATACTGA	TAATTCCAGT	TTGTCACCAC	CACCTGCTAA	ATTATCTGTT	240
GTCAGTTTTG	CCCCCTCCTC	CAATGAGGTT	GAAACAACAA	GCCTCAATGA	TGTTACTTTA	300
AGCTTACTCC	CTTCAAACGA	AACAGAAAAA	ACTAAAATCA	CTATAGTAAA	AACCTTCAAT	360
GCTTCAGGCG	TCAAACCCCA	GAGAAATATC	TGCAATTTGT	CATCTATTTG	CAATGACTCA	420
GCATTTTTTA	GAGGTGAGAT	CATGTTTCAA	TATGATAAAG	AAAGCACTGT	TCCCCAGAAT	480
CAACATATAA	CGAATGGCAC	CTTAAGTGA	GTCCTGTCTC	TAAGTGAATT	AAAACGCTCA	540
GAGCTCAACA	AAACCCTGCA	AACCCTAAGT	GACCTTACT	TTATAATGTG	TGCTACAGCA	600
GAGGCCCAAA	GCACATTAAA	TTGTACATTC	ACAATAAAAC	TGAATAATAC	AATGAATGCA	660
TGTGCTGCAA	TAGCCGCTTT	GGAAAGAGTA	AAGATTCGAC	CAATGGAACA	CTGCTGCTGT	720
TCTGTCAGGA	TACCCTGCCC	TTCTCCCCA	GAAGAGTTGG	GAAAGCTTCA	GTGTGACCTG	780
CAGGATCCCA	TTGTCGTGCT	TGCTGACCAT	CCACGTGGCC	CACCATTTTC	TTCCAGCCAA	840
TCCATCCCAG	TGGTGCCTCG	GGCCACTGTG	CTTTCCAGG	TCCCCAAAGC	TACCTCTTTT	900
GCTGAGCCTC	CAGATTATTC	ACCTGTGACC	CACAATGTTT	CCTCTCCAAT	AGGGGAGATT	960
CAACCCCTTT	CACCCAGCC	TTAGCTCCC	ATAGCTTCCA	GCCCTGCCAT	TGACATGCCC	1020
CCACAGTCTG	AAACGATCTC	TTCCCCTATG	CCCCAAACCC	ATGTCTCCGG	CACCCACCT	1080
CCTGTGAAAG	CCTCATTTTC	CTCTCCCACC	GTGTCTGCCC	CTGCGAATGT	CAACACTACC	1140
AGCGCACCTC	CTGTCCAGAC	AGACATCGTC	AACACCAGCA	GTATTTCTGA	TCTTGAGAAC	1200
CAAGTGTTGC	AGATGGAGAA	GGCTCTGTCC	TTGGGCAGCC	TGGAGCCTAA	CCTCGCAGGA	1260
GAAATGATCA	ACCAAGTCAG	CAGACTCCTT	CATTCCCCGC	CTGACATGCT	GGCCCCCTCTG	1320
GCTCAAAGAT	TGCTGAAAGT	AGTGGATGAC	ATTGGCCTAC	AGCTGAACTT	TTCAAACACG	1380
ACTATAAGTC	TAACCTCCCC	TTCTTTGGCT	CTGGCTGTGA	TCAGAGTGAA	TGCCAGTAGT	1440
TTCAACACAA	CTACCTTTGT	GGCCCAAGAC	CCTGCAAATC	TTCAGGTTTC	TCTGGAAACC	1500
CAAGCTCCTG	AGAACAGTAT	TGGCACAATT	ACTCTTCCTT	CATCGCTGAT	GAATAATTTA	1560
CCAGCTCATG	ACATGGAGCT	AGCTTCCAGG	GTTCTGATCA	ATTTTTTTGA	AACACCTGCT	1620
TTGTTTTCAGG	ATCCTTCCCT	GGAGAACCCT	TCTCTGATCA	GCTACGTCAT	ATCATCGAGT	1680
GTTGCAAACC	TGACCGTCAG	GAAC'TTGACA	AGAAACGTGA	CAGTCACATT	AAAGCACATC	1740
AACCCGAGCC	AGGATGAGTT	AACAGTGAGA	TGTGTATTTT	GGGACTTGGG	CAGAAATGGT	1800
GGCAGAGGAG	GCTGGTCAGA	CAATGGCTGC	TCTGTCAAAG	ACAGGAGATT	GAATGAAACC	1860
ATCTGTACCT	GTAGCCATCT	AACAAGCTTC	GGCGTTCTGC	TGGACCTATC	TAGGACATCT	1920
GTGCTGCCTG	CTCAAATGAT	GGCTCTGACG	TTCATTACAT	ATATTGGTTG	TGGGCTTTCA	1980
TCAATTTTTT	TGTCAGTGAC	TCTTGTAAAC	TACATAGCTT	TTGAAAAGAT	CCGGAGGGAT	2040
TACCCCTTCCA	AAATCCTCAT	CCAGCTGTGT	GCTGCTCTGC	TTCTGCTGAA	CCTGGTCTTC	2100
CTCCTGGACT	CGTGGATTGC	TCTGTATAAG	ATGCAAGGCC	TCTGCATCTC	AGTGGCTGTA	2160
TTTTCTTCATT	ATTTTCTCTT	GGTCTCATT	ACATGGATGG	GCCTAGAAGC	ATTCCATATG	2220
TACCTGGCCC	TTGTCAAAGT	ATTTAATACT	TACATCCGAA	AATACATCCT	TAAATTCTGC	2280
ATTGTGCGTT	GGGGGGTACC	AGCTGTGGTT	GTGACCATCA	TCCTGACTAT	ATCCCCAGAT	2340
AACTATGGGC	TTGGATCCTA	TGGGAAATTC	CCCAATGGTT	CACCGGATGA	CTTCTGCTGG	2400
ATCAACAACA	ATGCAGTATT	CTACATTACG	GTGGTGGGAT	ATTTCTGTGT	GATATTTTTG	2460
CTGAACGTCA	GCATGTTTCA	TGTGGTCTCG	GTTTCAGCTCT	GTCGAATTAA	AAAGAAGAAG	2520
CAACTGGGAG	CCCAGCGAAA	AACCAGTATT	CAAGACCTCA	GGAGTATCGC	TGGCCTTACA	2580
TTTTTACTGG	GAATAACTTG	GGGCTTTGCC	TTCTTTGCCT	GGGGACCAGT	TAACGTGACC	2640
TTCATGTATC	TGTTTGCCAT	CTTTAATACC	TTACAAGGAT	TTTTTCATATT	CATCTTTTAC	2700

FIG. 1

TGTGTGGCCA	AAGAAAATGT	CAGGAAGCAA	TGGAGGCGGT	ATCTTTGTTG	TGGAAAGTTA	2760
CGGCTGGCTG	AAAATTCTGA	CTGGAGTAAA	ACTGCTACTA	ATGGTTTAAA	GAAGCAGACT	2820
GTAAACCAAG	GAGTGTCCAG	CTCTTCAAAT	TCCTTACAGT	CAAGCAGTAA	CTCCACTAAC	2880
TCCACCACAC	TGCTAGTGAA	TAATGATTGC	TCAGTACACG	CAAGCGGGAA	TGGAAATGCT	2940
TCTACAGAGA	GGAATGGGGT	CTCTTTTAGT	GTTTCAGAAATG	GAGATGTGTG	CCTTCACGAT	3000
TTCACTGGAA	AACAGCACAT	GTTTAAACGAG	AAGGAAGATT	CCTGCAATGG	GAAAGGCCGT	3060
ATGGCTCTCA	GAAGGACTTC	AAAGCGGGGA	AGCTTACACT	TTATTGAGCA	AATGTGATTC	3120
CTTTCTTCTA	AAATCAAAGC	ATGATGCTTG	ACAGTGTGAA	ATGTCCAATT	TTACCTTTTA	3180
CACAATGTGA	GATGTATGAA	AATCAACTCA	TTTTATTCTC	GGCAACATCT	GGAGAAGCAT	3240
AAGCTAATTA	AGGGCGATGA	TTATTATTAC	AAGAAGAAAC	CAAGACATTA	CACCATGGTT	3300
TTTAGACATT	TCTGATTTGG	TTTCTTATCT	TTCATTTTAT	AAGAAGGTTG	GTTTTAAACA	3360
ATACACTAAG	AATGACTCCT	ATAAAGAAAA	CAAAAAAAGG	TAGTGAACCT	TCAGCTACCT	3420
TTTAAAGAGG	CTAAGTTATC	TTTGATAACA	TCATATAAAG	CAACTGTTGA	CTTCAGCCTG	3480
TTGGTGAGTT	TAGTTGTGCA	TGCCTTTGTT	GTATATAAGC	TAAATTCTAG	TGACCCATGT	3540
GTCAAAAATC	TTACTTCTAC	ATTTTTTTGT	ATTTATTTTC	TACTGTGTAA	ATGTATTCCCT	3600
TTGTAGAATC	ATGGTTGTTT	TGTCTCACGT	GATAATTGAG	AAAATCCCTG	CTCGTTCCGC	3660
AAATCCTAAA	GCTCCTTTTG	GAGATGATAT	AGGATGTGAA	ATACAGAAAC	CTCAGTGAAA	3720
TCAAGAAATA	ATGATCCCAG	CCAGACTGAG	AAAATGTAAG	CAGACAGTGC	CACAGTTAGC	3780
TCATACAGTG	CCTTTGAGCA	AGTTAGGAAA	AGATGCCCCC	ACTGGGCAGA	CACAGCCCTA	3840
TGGGTCATGG	TTTGACAAAC	AGAGTGAGAG	ACCATATTTT	AGCCCCACTC	ACCTCTTTGG	3900
GTGCACGACC	TGTACAGCCA	AACACAGCAT	CCAATATGAA	TACCCATCCC	CTGACCGCAT	3960
CCCCAGTAGT	CAGATTATAG	AATCTGCACC	AAGATGTTTA	GCTTTATACC	TTGGCCACAG	4020
AGAGGGATGA	ACTGTCATCC	AGACCATGTG	TCAGGAAAAT	TGTGAACGTA	GATGAGGTAC	4080
ATACACTGCC	GCTTCTCAAA	TCCCCAGAGC	CTTTAGGAAC	AGGAGAGTAG	ACTAGGATTC	4140
CTTCTCTTAA	AAAGGTACAT	ATATATGGAA	AAAAATCATA	TTGCCGTTCT	TTAAAAGGCA	4200
ACTGCATGGT	ACATTGTTGA	TTGTTATGAC	TGGTACACTC	TGGCCCAGCC	AGAGCTATAA	4260
TTGTTTTTTT	AATGTGTCTT	GAAGAATGCA	CAGTGACAAG	GGGAGTAGCT	ATTGGGAACA	4320
GGGAAGTGTC	CTACACTGCT	ATTGTTGCTA	CATGTATCGA	GCCTTGATTG	TCCTAGTTTA	4380
TATACAGGGT	CTATCTTGCT	TCCTACCTAC	ATCTGCTTGA	GCAGTGCCTC	AAGTACATCC	4440
TTATTAGGAA	CATTTCAAAC	CCCTTTTAGT	TAAGTCTTTC	ACTAAGGTTT	TCTTGTCATAT	4500
ATTTCAAGTG	AATGTTGGAT	CTCAGACTAA	CCATAGTAAT	AATACACATT	TCTGTGAGTG	4560
CTGACTTGTC	TTTGCAATAT	TTCTTTTCTG	ATTTATTTAA	TTTTCTTGTA	TTTATATGTT	4620
AAAATCAAAA	ATGTTAAAAA	CAATGAAATA	AATTTGCAGT	TAAGA		

GPR64 AMINO ACID SEQUENCE (SEQ ID NO:2)

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.421137
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805,
 828-850, 858-880
 Cellular Localization: plasma membrane

1	11	21	31	41	51	
MVFSVRQCGH	VGRTEEVLLT	FKIFLVIICL	HVVLVTSLEE	DTDNSSLSP	PAKLSVVSFA	60
PSSNEVETTS	LNDVTLSELLP	SNETEKTKIT	IVKTFNASGV	KPQRNICNLS	SICNDSAFFR	120
GEIMFQYDKE	STVPQNQHIT	NGTLTGVLSL	SELKRSELNK	TLQTLSETYF	IMCATAEAQS	180
TLNCTFTIKL	NNTMNACAAI	AALERVKIRP	MEHCCCSVRI	PCPSSPEELG	KLQCDLQDPI	240
VCLADHPRGP	PFSSSQSIPV	VPRATVLSQV	PKATSFAEPP	DYSPVTHNVP	SPIGEIQPLS	300
PQPSAPIASS	PAIDMPPQSE	TISSPMPQTH	VSGTPPPVKA	SFSSPTVSAP	ANVNTTSAPP	360
VQTDIVNTSS	ISDLENQVLQ	MEKALSLGSL	EPNLAGEMIN	QVSRLHHSPP	DMLAPLAQRL	420
LKVVDIDGLQ	LNFSNTTISL	TSPSLALAVI	RVNASSFNNT	TFVAQDPANL	QVSLETQAPE	480
NSIGTITLPS	SLMNNLPAHD	MELASRVQFN	FFETPALFQD	PSLENLSLIS	YVISSSVANL	540

FIG. 1

TVRNLTRNVT	VTLKHINPSQ	DELTVRVCFW	DLGRNGGRGG	WSDNGCSVKD	RRLNETICTC	600
SHLTSFGVLL	DLSRTSVLPA	QMMALTFITY	IGCGLSSIFL	SVTLVTYIAF	EKIRRDYPSK	660
ILIQLCALL	LLNLVFLDS	WIALYKMQGL	CISVAVFLHY	FLLVSFTWMG	LEAFHMYLAL	720
VKVFTYIRK	YILKFCIVGW	GVPVVVTII	LTISPDNYGL	GSYGKFPNGS	PDDFCWINNN	780
AVFYITVVG	FCVIFLLNVS	MFIVVLVQLC	RIKKKKQLGA	QRKTSIQDLR	SIAGLTFLLG	840
ITWGAFFAW	GPVNVTFMYL	FAIFNTLQGF	FIFIFYCVAK	ENVRKQWRRY	LCCGKLRLAE	900
NSDWSKTATN	GLKKQTVNQG	VSSSSNSLQS	SSNSTNSTTL	LVNNDCSVHA	SGNGMASTER	960
NGVSFSVQNG	DVCLHDFTGK	QHMFNEKEDS	CNGKGRMALR	RTSKRGSLSHF	IEQM	

FIG. 1

**NUCLEOTIDE AND AMINO ACID SEQUENCES OF GPR64 ANTIBODY
CLONES (CDR regions are shown bolded and underlined.)**

NUCLEOTIDE SEQUENCES

SEQ ID NO:3: GPR64-1 Heavy Chain Variable Region:

GATGTGCAGCTTCAGGAGTCGGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTG
TCCCTCACCTGCACTGTCACT**GGCTACTCAATCACCAGTGATTATGCCTGGAA**
CTGGATCCGGCAGTTTCCAGGAAACAACTGGAGTGGCTGGGCTACATAAGCT
TCAATGATAACACTAACTACAACCCATCTCTCAAAAGTCGAATCTCTATCAC
TCGAGACACATCCAAGAACCAGTTCTTCCTGCAGTTGAATTCTGTGACTACTGA
GGACACAGCCACATATTACTGTACAAGG**AGGGTGGACTACT**GGGGTCAAGGA
ACCTCAGTCACCGTCTCCTCA

SEQ ID NO:4: GPR64-1 Light Chain Variable Region

GATGTTGTGATGACCCAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAA
GCCTCCATCTCTTGC**AGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACA**
ACTATTTACATTGGTATTTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCT
ACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGA
TCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGG
AGTTTATTTCTGCT**TCTCAAAGTACACATGTTCCGTGGACGTT**CGGTGGAGGCA
CCAAGCTGGAAATCAAA

SEQ ID NO:5: GPR64-16 Heavy Chain Variable Region

CAGGTTACTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTC
AGTCTGACTTGTCTTTCTCT**GGGTTTTCACTGAGCACTTCTGGTGTGGGTGT**
GAGCTGGATTTCGTCAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTT
ACTGGGATGATGATAAGCGCTATAACCCATCCCTGAAGAGCCGGCTCACAA
TCTCCAAGGATACCTCCAGAAACCAGGTATTCCTCAAGATCACCAGTGTGGACA
CTGCAGATACTGCCACATACTACTGTGCTCGA**AGAGTATTCATTATTACGGCC**
TTTGACTACTGGGGCCAAGGCACCACTCTCACAGTCTCCTCA

SEQ ID NO:6: GPR64-16 Light Chain Variable Region

GATATCCAGATGACACAGACTACATCCTCCCTGTCTGCCTCTCTGGGAGACAGA
GTCACCATCAGTTGCAGGGCAAGTCAGGACATTAGCAATTACTTAACTGGT
ATCAGCAGAAACCAGATGGAAGTGTAACTCCTGATCTACTACACATCAA
ACTTACACTCAGGAGTCCCATCAAGGTTCAAGTGGCAGTGGGTCTGGAGCAGATTAT
TCTCTACCATTTGGCAACCTGGAGCAAGAAGATATTGCCACTTACTTTTGCCAA
CAGGGTAATACGCTTCCTTGGACGTTTCGGTGGAGGCACCAAGCTGGAAATCA
AA

FIG. 2

SEQ ID NO:7: GPR64-18 HEAVY CHAIN VARIABLE REGION

CAGGTTTCTCTGAAAGAGTCTGGCCCTGGGATATTGCAGCCCTCCCAGACCCTC
AGTCTGACTTGTTCTTTCTCTGGGTTTTCACTGAGCACTTCTGGTATGGGTGTGA
GCTGGATTTCGTCAGCCTTCAGGAAAGGGTCTGGAGTGGCTGGCACACATTACT
GGGATGATGACAAGCGCTATAACCCATCCCTGAAGAGCCGGCTCACAATCTCC
AAGGATACCTCCAGCAACCTGGTATTCCTCAAGATCACCAGTGTGGACACTGCA
GATACTGCCACATACTACTGTGCTCGAAGGGGAAGTACGACGTGATTACTATGCT
ATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA

SEQ ID NO:8: GPR64-18 Light Chain Variable Region

AGTATTGTGATGACCCAGACTCCCAAATTCCTGCTTGTCTCAGCAGGAGACAGG
ATTACCATAGCCTGCAGGGCCAGTCAGAGTGTGAGTAATGATGTAGCTTGGT
ACCAACAGAAGCCAGGGCAGTCTCCTAAACTGCTGATAAACTATACATCCAAT
CGCTACACTGGAGTCCCTGATCGCTTCACTGGCAGTGGATATGGGACGGATT
CACTTTCACCATCAGCACTGTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCA
GCAGGCTTATAGCTCTCCGTGGACGTTTCGGTGGAGGCACCAAGCTGGAAATC
AAACGG

SEQ ID NO:9: GPR64-20 Heavy Chain Variable Region

GATGTGCAGCTTCAGGAGTCGGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTG
TCCCTCACCTGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAA
CTGGATCCGGCAGTTTCCAGGAAACAACTGGAGTGGATGGGCTACATAAGCT
ACAGTGATTACACTAGCTACAACCCATCTCTCAAAAGTCGAATCTCTATCAC
TCGAGACACATCCAAGAACCAGTTCTTCTGCAAGTGAATTCTGTGACTACTGA
GGACACAGCCACATATTACTGTGCAAGAAGGGTGGACTACTGGGGTCAAGGA
ACCTCAGTCACCGTCTCCTCA

SEQ ID NO:10: GPR64-20 Light Chain Variable Region

GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAA
GCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACA
CCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCT
ACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGA
TCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGG
AGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTGGACGTTTCGGTGGAGGCA
CCACGCTGGAAATCAAA

SEQ ID NO:11: GPR64-48 Heavy Chain Variable Region

GATGTGCAGCTTCAGGAGTCGGGACCTGGCCTGGTGAAACCTTCTCAGTCTCTG
TCCCTCACCTGCACTGTCACTGGCTACTCAATCACCAGTGATTATGCCTGGAA
CTGGATCCGGCAGTTTCCAGGAAACAACTGGAGTGGATGGGCTACATAAGCT
TCAGTGATAGCACTAGCTACAACCCATCTCTCAAAAGTCGAATCTCTATCAC
TCGAGACACATCCAAGAACCAGTTCTTCTGCAAGTGAATTCTGTGACTACTGA
GGACACAGCCACATATTACTGTGCAAGAAGGGGGGACTACTGGGGTCAAGGA
ACCTCAGTCACCGTCTCCTCA

FIG. 2

SEQ ID NO:12: GPR64-48 Light Chain Variable Region

GATGTTGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAAGTCTTGGAGATCAA
GCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACA
CCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCT
ACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAAGTGGCAGTGGA
TCAGGGACAGATTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGG
AGTTTATTTCTGCTCTCAAAGTACACATCTTCCGTGGACGTTTCGGTGGAGGCA
CCAAGCTGGAAATCAAA

AMINO ACID SEQUENCES

SEQ ID NO:13: GPR64-1 Heavy Chain Variable Region

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWLGYISFND
NTNYPNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCTRRVDYWGQGSVTVS
S

SEQ ID NO:14: GPR64-1 Light Chain Variable Region

DVVMQTQTPLSLPVSLGDQASISCRSSQSLVHSNGNNYLHWYLQKPGQSPKLLIYK
VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEI
K

SEQ ID NO:15: GPR64-16 Heavy Chain Variable Region

QVTLKESGPGILQPSQTLSTCSFSGFSLSTSSGVGVSWIRQPSGKGLEWLAHIYWD
DDKRYNPSLKSRLTISKDTSRNQVFLKITSVDTADTATYYCARRRVFIITAFDYWGQ
GTTLTVSS

SEQ ID NO:16: GPR64-16 Light Chain Variable Region

DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSNLHS
GVPSRFSGSGSGADYSLTIGNLEQEDIATYFCQOGNTLPWTFGGGTKLEIK

SEQ ID NO:17: GPR64-18 Heavy Chain Variable Region

QVSLKESGPGILQPSQTLSTCSFSGFSLSTSSGMGVSWIRQPSGKGLEWLAHIYWD
DDKRYNPSLKSRLTISKDTSSNLVFLKITSVDTADTATYYCARREVRRDYAMDY
WGQGSVTVSS

SEQ ID NO:18: GPR64-18 Light Chain Variable Region

SIVMTQTPKFLLVSAGDRITIACRASQSVNDVAWYQQKPGQSPKLLINYTSNRYT
GVPDRFTGSGYGTDFTFITVQAEDLAVYFCQQAYSSPWTFGGGTGLEIK

FIG. 2

SEQ ID NO:19: GPR64-20 Heavy Chain Variable Region

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYS
DYTSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARRRDYWGQGTSVTV
SS

SEQ ID NO:20 GPR64-20 Light Chain Variable Region

DVVMQTQTPSLPVS LGDQASISCRSSQSLVHSNGNTYLHWY LQKPGQSPKLLIYK
VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTTLEIK

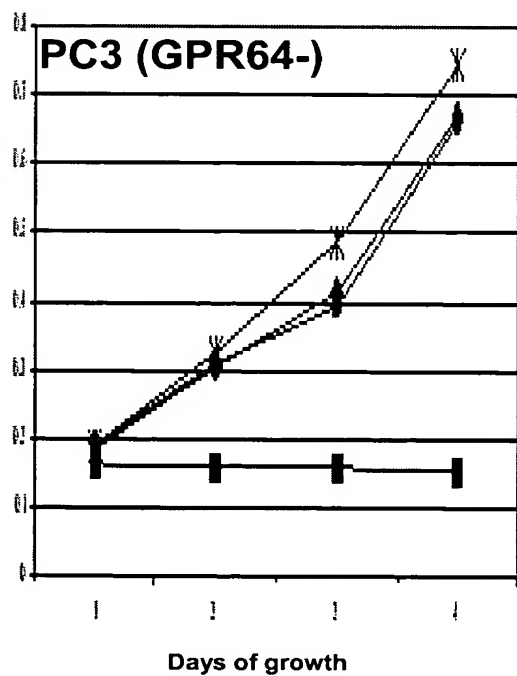
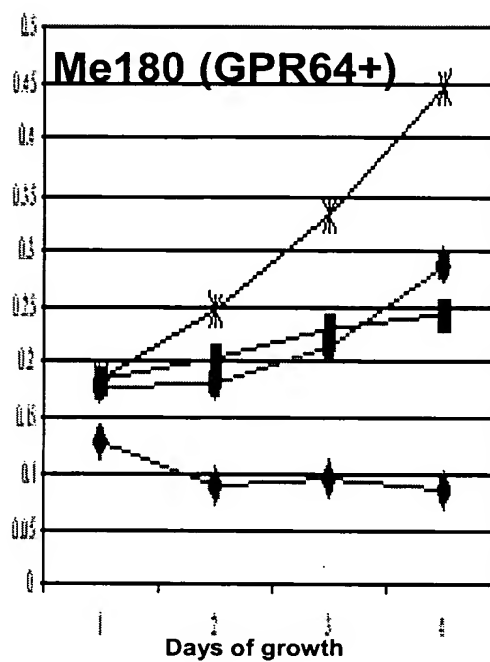
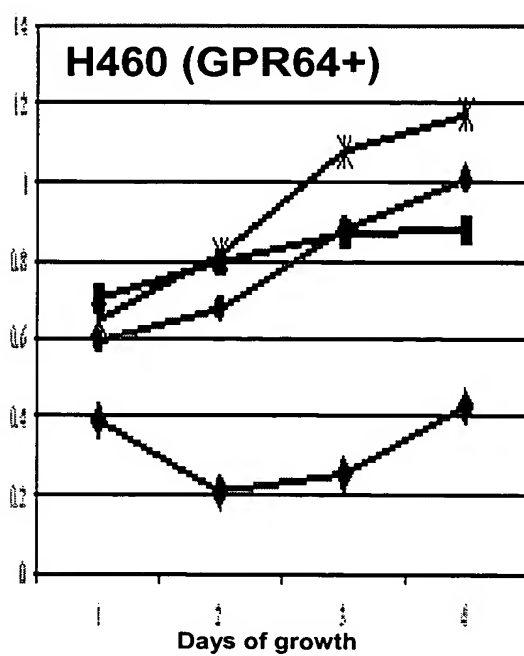
SEQ ID NO:21: GPR64-48 Heavy Chain Variable Region

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISFSD
STSYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARRRGDYWGQGTSVTVS
S

SEQ ID NO:22: GPR64-48 Light Chain Variable Region

DVVMQTQTPSLPVS LGDQASISCRSSQSLVHSNGNTYLHWY LQKPGQSPKLLIYK
VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHLPWTFGGGTKLEIK

FIG. 2



4 Days Growth

- HKSP-2
- *— H2R-1X
- ◆— OAM6 #110X
- OAM6 #111

FIG. 3

GPR+ Cells

<u>RNA+</u>	<u>FACS</u> <u>expression</u>	<u>MTT</u> <u>effect</u>
ME180	+	+
H460	+	+
H520	+	+
C32	+	-
DU145	+	-

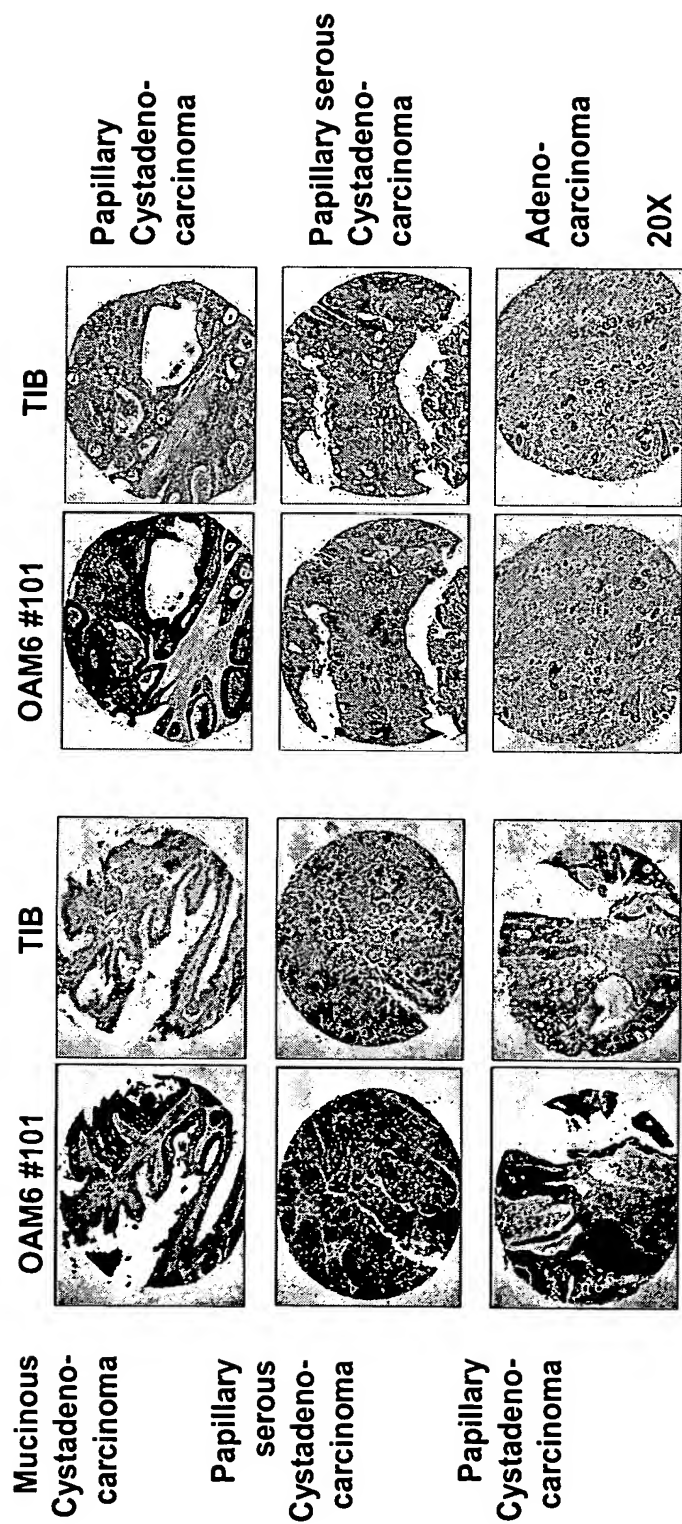
GPR64- Cells

<u>RNA+</u>	<u>FACS</u> <u>expression</u>	<u>MTT</u> <u>effect</u>	<u>RNA-</u>	<u>FACS</u> <u>expression</u>	<u>MTT</u> <u>effect</u>
BT474	-	-	HT1376	ND	-
MCF7	-	-	SW780	-	+
NW231	-	-	HCT116	ND	-
H358	-	-	SW620	ND	-
Calu6	-	-	U87	-	-
SKOV3	-	-	A549	-	-
LnCAP	-	+	A375	-	-
			C8161	-	-
			ES2	-	-
			OV-90	ND	-
			OVCAR3	-	-
			PA-1	ND	-
			PC3	-	-

Fig. 4

Mab	FACS (nM)	IHC	IF	Biacore	Isotype	Mab	FACS (nM)	IHC	IF	Biacore	Isotype
61a	0.7288	3+	2+	1.09E-09	2b	85a	38.2	2+	2+	2.78E-09	
62a	2.736	2+	2+	1.73E-09	2b	86a	97.98	neg	1+		2a
65a	1.371	2+	2+	1.48E-09	2b	87a	77.04	neg	-		
68a	6.15	2+	1+		1	88a	37.51	neg			
70a	1.831	3+	2+	1.22E-09	2b	89a	107	neg			
80a	0.4032	2+	1+		1	90a	194.6	2+	2+		
67a	246.1	2+	-			91a	4.252	3+	2+		
69a	295.6	neg	-			93a	1.269	2+	1+	8.01E-09	2a
71a	8.159	2+	-		1	94a	87.84	2+	2+	1.66E-07	
72a	130.8	neg	-			95a	28.81	3+	2+	6.29E-10	2b
74a	442.6	2+	-			96a	22.77	2+	-		2a
75a	102.4	2+	2+	9.68E-09		97a		nd			
76a	0.8313	2+	2+	1.62E-10	2a	98a	186.1	nd			
77a	0.9765	3+	1+	2.07E-09	1	99a	10.96	2+	2+	6.97E-09	1
78a	8.955	2+	1+	4.06E-11	2a	100a	42.1	2+	2+	1.81E-09	2a
79a	5.299	3+	1+			101a	4.939	3+	2+	1.46E-10	2a
81a	0.0585	2+	1+	1.38E-08	1	102a	117.2	nd	-		1
82a	5.829	2+	2+	1.61E-09		103a		nd	-		2a
83a	124.7	2+	-			79b		3+			
84a	113.6	2+	-		2a	77b		nd			
18b1	~4.0	2+	1+	2.83E-09	1	104		nd			

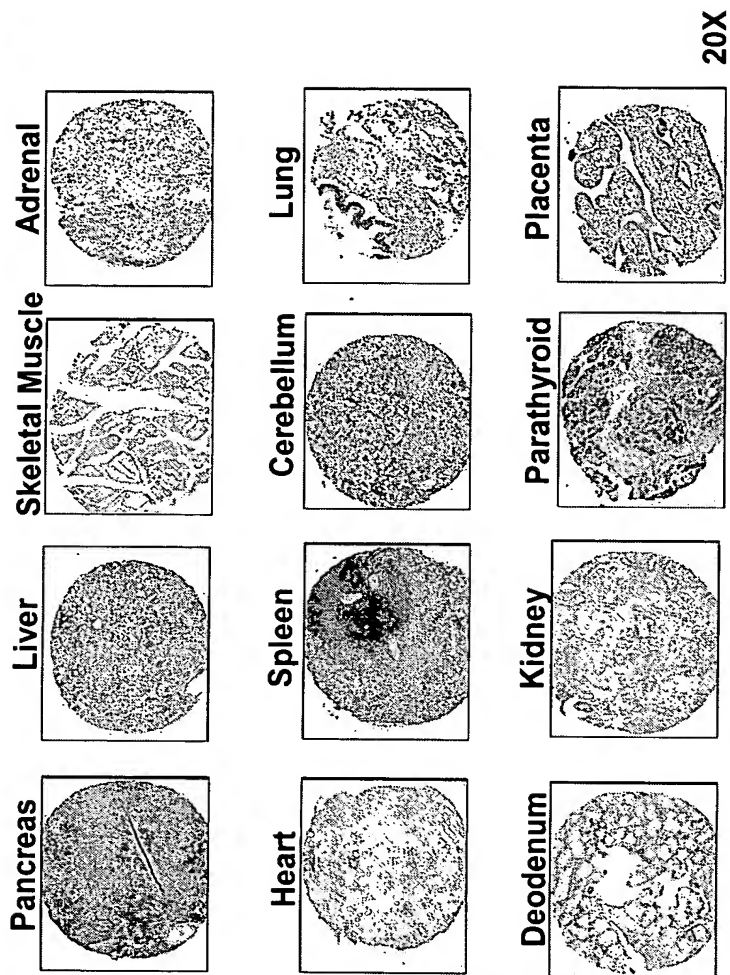
Fig. 5



OAM6 #101	4+	3+	2+	1+	+/-	neg	Total
Omental mets	-	8	8	3	-	-	19/19
Ovarian cancer	2	1	-	2	1	-	6/6

FIG. 6

Normal Tissues



OAM6 #101



Omental mets

FIG. 7

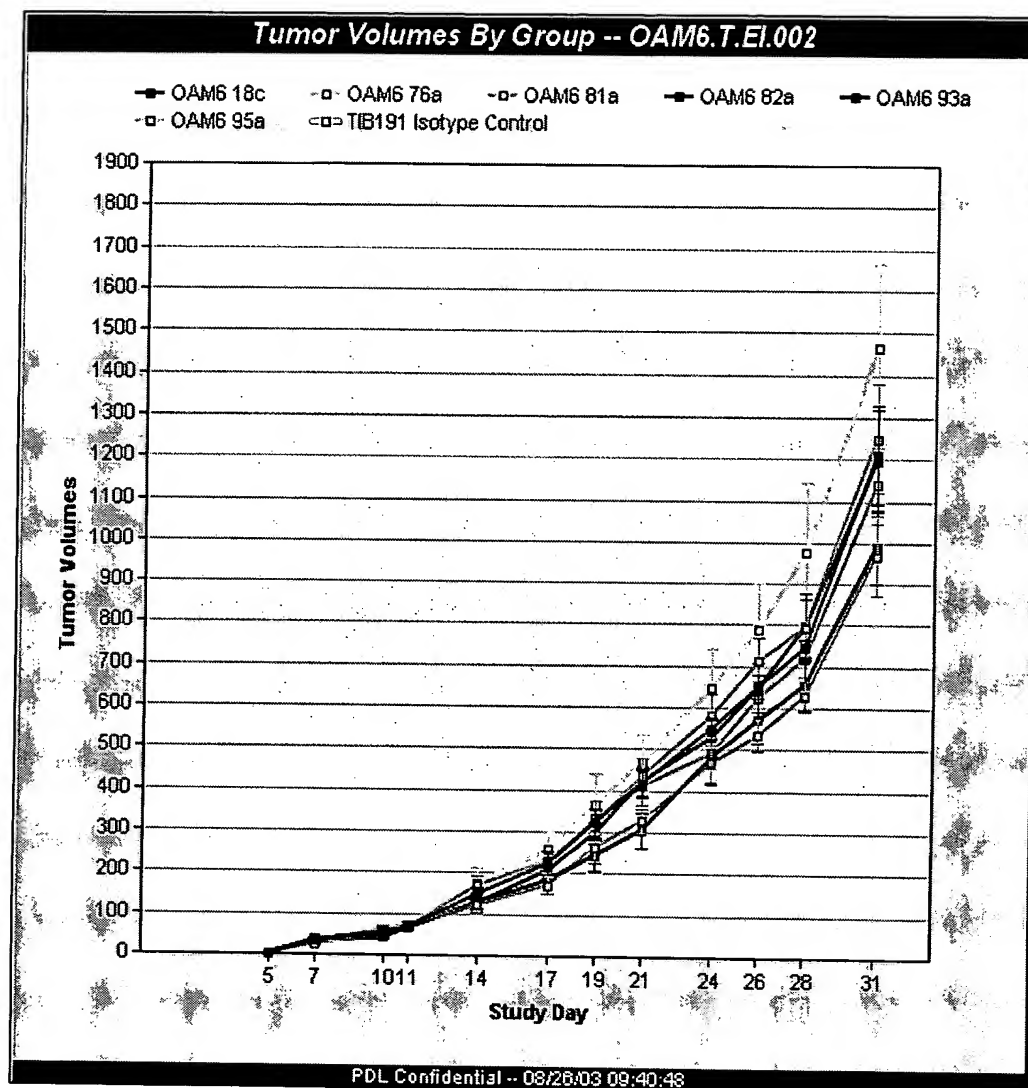


FIG. 8



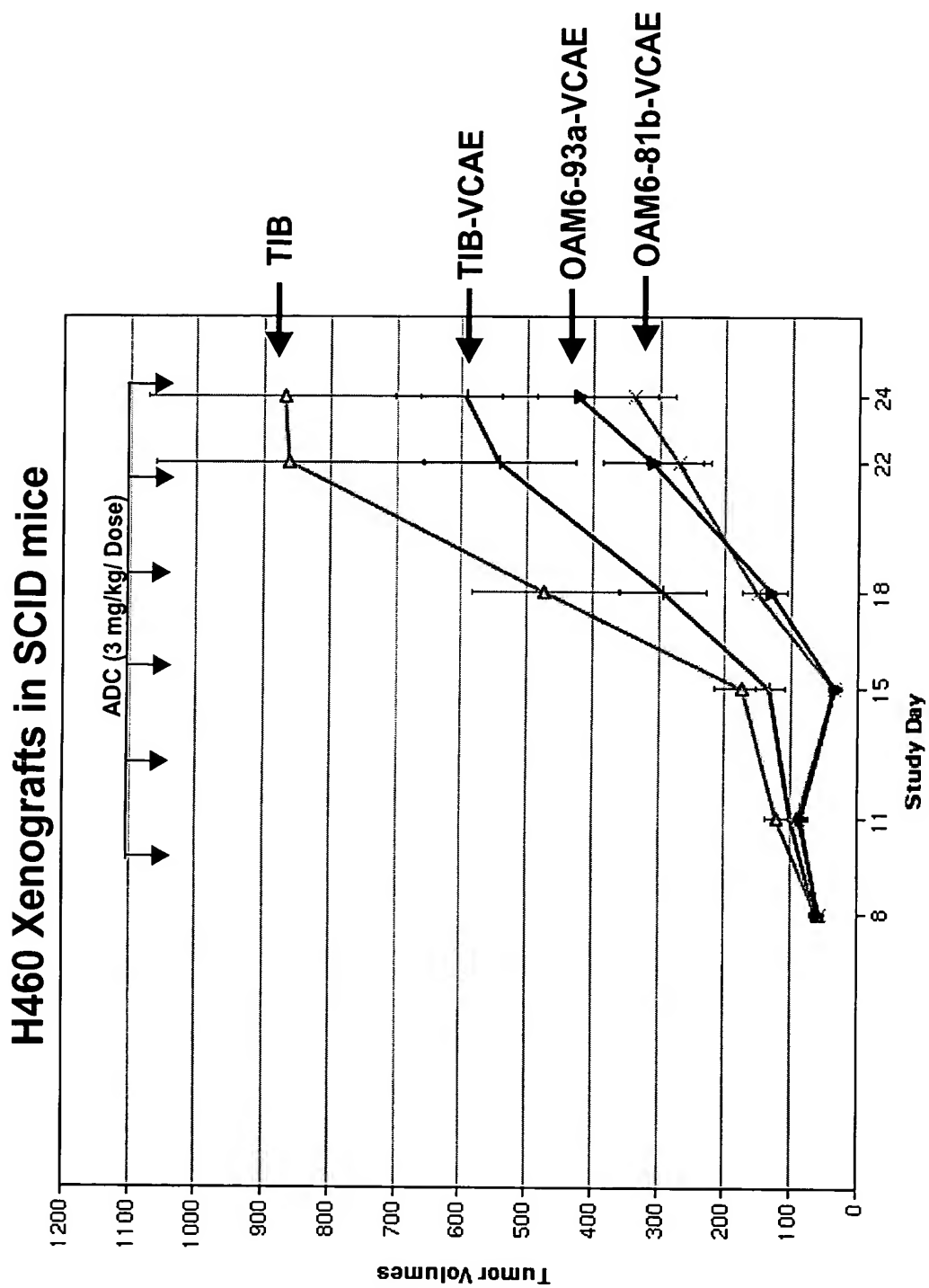


FIG. 10